SWANSON & BRATSCHUN, L.L.C.
8210 SouthPark Terrace
Littleton, Colorado 80120
Telephone (303) 268-0066
Facsimile (303) 268-0065
e-Mail: firm@sbiplaw.com

FACSIMILE COVER PAGE

TO: Robert Mondesi

COMPANY: United States Patent and Trademark Office

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RE: **U.S. Application Serial No.: 10/031,496**
Title: CELLOBIOHYDROLASE 1 GENE AND IIMPROVED VARIANTS
Filed: January 14, 2002
Art Unit: 1652
Confirmation No.: 6834
Attorney Docket No.: NREL 99-45

Dear Mr. Mondesi:

Please refer to the attached Proposed Amendment in regard to the above-referenced matter.

Thank you.

Regards,

Paul J. Prendergast

Attorney Docket No. NREL 99-45

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT:	ADNEY, ET AL.	EXAMINER:	MONDESI, ROBERT
SERIAL NO.:	10/031,496		
FILED:	JANUARY 14, 2002	ART UNIT:	1652
TITLE:	CELLOBIOHYDROLASE 1 GENE AND IMPROVED VARIANTS	CONF. NO.:	6834

Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

PROPOSED AMENDMENT

Sir:

In response to the November 7, 2007 teleconference with the Examiner, Applicants propose the following two options for addressing the Examiner's concern regarding the numbering of the residues described in the claims/specification and the respective residues in SEQ ID NO: 5:

1. Add a wherein clause to each of the independent claims indicating the signal sequence is removed and the residue count starts at the mature protein. Such an amendment is supported by the originally filed specification at least on page 5, first and second paragraphs, as well as Figure 1 which shows the coding sequence for the fusion protein (17 amino acid signal sequence with the 498 amino acid glucoamylase). Figure 1 clearly identifies the nucleic acids encoding the signal sequence distinct from the nucleic acids encoding the mature protein.

As such, Claim 6 could be amended to read as follows:

> 6. A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase mutated with respect to a wild-type cellobiohydrolase represented by SEQ ID NO: 5, the mutation providing means for improving cellobiohydrolase functionality with respect to the wild-type cellobiohydrolase functionality,
> wherein the functionality is thermostability, enzymatic activity, catalytic activity, product inhibition, glycosylation, and/or peptide strain,